



SEQUENCE LISTING

<110> Kahn, C. Ronald
Zhu, Jianhua

<120> MODULATING THE RAD-NM23 INTERACTION

<130> 10276-017002

<140> US 10/074,694

<141> 2002-02-12

<150> US 09/053,967

<151> 1998-04-02

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 308

<212> PRT

<213> Homo sapiens

<400> 1

Met	Thr	Leu	Asn	Gly	Gly	Gly	Ser	Gly	Ala	Gly	Gly	Ser	Arg	Gly	Gly	
1				5					10					15		
Gly	Gln	Glu	Arg	Glu	Arg	Arg	Arg	Gly	Ser	Thr	Pro	Trp	Gly	Pro	Ala	
			20					25					30			
Pro	Pro	Leu	His	Arg	Arg	Ser	Met	Pro	Val	Asp	Glu	Arg	Asp	Leu	Gln	
		35					40					45				
Ala	Ala	Leu	Thr	Pro	Gly	Ala	Leu	Thr	Ala	Ala	Ala	Ala	Gly	Thr	Gly	
	50					55					60					
Thr	Gln	Gly	Pro	Arg	Leu	Asp	Trp	Pro	Glu	Asp	Ser	Glu	Asp	Ser	Leu	
65					70				75						80	
Ser	Ser	Gly	Gly	Ser	Asp	Ser	Asp	Glu	Ser	Val	Tyr	Lys	Val	Leu	Leu	
			85					90						95		
Leu	Gly	Ala	Pro	Gly	Val	Gly	Lys	Ser	Ala	Leu	Ala	Arg	Ile	Phe	Gly	
		100						105					110			
Gly	Val	Glu	Asp	Gly	Pro	Glu	Ala	Glu	Ala	Ala	Gly	His	Thr	Tyr	Asp	
	115						120					125				
Arg	Ser	Ile	Val	Val	Asp	Gly	Glu	Glu	Ala	Ser	Leu	Met	Val	Tyr	Asp	
	130					135					140					
Ile	Trp	Glu	Gln	Asp	Gly	Gly	Arg	Trp	Leu	Pro	Gly	His	Cys	Met	Ala	
145				150					155					160		
Met	Gly	Asp	Ala	Tyr	Val	Ile	Val	Tyr	Ser	Val	Thr	Asp	Lys	Gly	Ser	
			165					170						175		
Phe	Glu	Lys	Ala	Ser	Glu	Leu	Arg	Val	Gln	Leu	Arg	Arg	Ala	Arg	Gln	
		180						185					190			
Thr	Asp	Asp	Val	Pro	Ile	Ile	Leu	Val	Gly	Asn	Lys	Ser	Asp	Leu	Val	
	195						200					205				
Arg	Ser	Arg	Glu	Val	Ser	Val	Asp	Glu	Gly	Arg	Ala	Cys	Ala	Val	Val	
	210					215				220						
Phe	Asp	Cys	Lys	Phe	Ile	Glu	Thr	Ser	Ala	Ala	Leu	His	His	Asn	Val	
225					230					235					240	

Gln Ala Leu Phe Glu Gly Val Val Arg Gln Ile Arg Leu Arg Arg Asp
 245 250 255
 Ser Lys Glu Ala Asn Ala Arg Arg Gln Ala Gly Thr Arg Arg Arg Glu
 260 265 270
 Ser Leu Gly Lys Lys Ala Lys Arg Phe Leu Gly Arg Ile Val Ala Arg
 275 280 285
 Asn Ser Arg Lys Met Ala Phe Arg Ala Lys Ser Lys Ser Cys His Asp
 290 295 300
 Leu Ser Val Leu
 305

<210> 2
 <211> 664
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(498)

<400> 2
 cag tcg cag ccg gcg gta aag cct tgt cat ctg aag ggg acc atg gcc 48
 Gln Ser Gln Pro Ala Val Lys Pro Cys His Leu Lys Gly Thr Met Ala
 1 5 10 15
 aac agt gag cgt acc ttc att gcc atc aag cct gat ggg gtc cag cgg 96
 Asn Ser Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg
 20 25 30
 ggg ctg gtg ggc gag atc atc aag cgg ttc gag cag aag ggg ttc cgc 144
 Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg
 35 40 45
 ctt gtt ggt ctg aag ttt ctg cag gct tca gag gac ctt ctc aag gag 192
 Leu Val Gly Leu Lys Phe Leu Gln Ala Ser Glu Asp Leu Leu Lys Glu
 50 55 60
 cac tac act gac ctg aag gac cgc ccc ttc ttt act ggc ctg gtg aaa 240
 His Tyr Thr Asp Leu Lys Asp Arg Pro Phe Phe Thr Gly Leu Val Lys
 65 70 75 80
 tac atg cac tca gga cca gtg gtt gct atg gtc tgg gag ggt ctg aat 288
 Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn
 85 90 95
 gtg gtg aag aca ggc cgc gtg atg ctt gga gag acc aac ccc gca gac 336
 Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp
 100 105 110
 tct aag cct ggg acc ata cga gga gac ttc tgc att caa gtt ggc agg 384
 Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg
 115 120 125
 aac atc att cat ggc agc gat tct gta aag agc gca gag aag gag atc 432
 Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys Glu Ile
 130 135 140

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agc ttg tgg ttt cag cct gag gag ctg gtg gag tac aag agc tgt gcg 480
Ser Leu Trp Phe Gln Pro Glu Glu Leu Val Glu Tyr Lys Ser Cys Ala
145                150                155                160

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cag aac tgg atc tat gag tgataggacg gtgccgggttt tctacctgct 528
Gln Asn Trp Ile Tyr Glu
                165

```

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tactcttggtt ctcacaggca ggggaccagc aaccctagat atttctggaa cttctttgac 588
ctggaaggaa cctttgggag ccgtgactcc ctgtgcagtg ttacgtgcca ctgttagatt 648
aaagtgttta atctgt 664

```

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<210> 3
<211> 166
<212> PRT
<213> Mus musculus

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```

<400> 3
Gln Ser Gln Pro Ala Val Lys Pro Cys His Leu Lys Gly Thr Met Ala
1      5      10      15
Asn Ser Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg
20     25     30
Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg
35     40     45
Leu Val Gly Leu Lys Phe Leu Gln Ala Ser Glu Asp Leu Leu Lys Glu
50     55     60
His Tyr Thr Asp Leu Lys Asp Arg Pro Phe Phe Thr Gly Leu Val Lys
65     70     75     80
Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn
85     90     95
Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp
100    105    110
Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg
115    120    125
Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys Glu Ile
130    135    140
Ser Leu Trp Phe Gln Pro Glu Glu Leu Val Glu Tyr Lys Ser Cys Ala
145    150    155    160
Gln Asn Trp Ile Tyr Glu
                165

```

```

<210> 4
<211> 670
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (73) ... (528)

```

```

<400> 4
cggccacgag gcggaatccc ttctgctctc ccagcgcagc gccgccgccc ggcccctcca 60
gcttcccgga cc atg gcc aac ctg gag cgc acc ttc atc gcc atc aag ccg 111
Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro
1      5      10

```

```

gac ggc gtg cag cgc ggc ctg gtg ggc gag atc atc aag cgc ttc gag 159
Asp Gly Val Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu
    15                20                25

cag aag gga ttc cgc ctc gtg gcc atg aag ttc ctc cgg gcc tct gaa 207
Gln Lys Gly Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu
    30                35                40                45

gaa cac ctg aag cag cac tac att gac ctg aaa gac cga cca ttc ttc 255
Glu His Leu Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe
                50                55                60

cct ggg ctg gtg aag tac atg aac tca ggg ccg gtt gtg gcc atg gtc 303
Pro Gly Leu Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val
                65                70                75

tgg gag ggg ctg aac gtg gtg aag aca ggc cga gtg atg ctt ggg gag 351
Trp Glu Gly Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu
                80                85                90

acc aat cca gca gat tca aag cca ggc acc att cgt ggg gac ttc tgc 399
Thr Asn Pro Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys
                95                100                105

att cag gtt ggc agg aac atc att cat ggc agt gat tca gta aaa agt 447
Ile Gln Val Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser
110                115                120                125

gct gaa aaa gaa atc agc cta tgg ttt aag cct gaa gaa ctg gtt gac 495
Ala Glu Lys Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp
                130                135                140

tac aag tct tgt gct cat gac tgg gtc tat gaa taagaggtgg acacaacagc 548
Tyr Lys Ser Cys Ala His Asp Trp Val Tyr Glu
                145                150

agtctccttc agcacggcgt ggtgtgtccc tggacacagc tcttcattcc attgacttag 608
aggcaacagg attgatcatt cttttataga gcatatttgc caataaagct tttggaagcc 668
ggg                                                    670

```

```

<210> 5
<211> 152
<212> PRT
<213> Homo sapiens

```

```

<400> 5
Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val
 1          5          10          15
Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly
    20          25          30
Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu Glu His Leu
    35          40          45
Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe Pro Gly Leu
    50          55          60
Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val Trp Glu Gly
65          70          75          80

```

[illegible]